

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:45:23 ; Search time 131 Seconds  
(without alignments)  
7281.517 Million cell updates/sec

Title: US-09-640-582a-1  
Perfect score: 1342  
Sequence: 1 cgttcgctccaccgaagatc.....caccgcgchcncctccacc 1342

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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2: /cgm2\_6/prodata/1/ina/5B COMB. seq.\*  
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4: /cgm2\_6/prodata/1/ina/6B COMB. seq.\*  
5: /cgm2\_6/prodata/1/ina/6C COMB. seq.\*  
6: /cgm2\_6/prodata/1/ina/6D COMB. seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1207	89.9	1792	4	US-09-086-436-40 Sequence 40, Appl
2	1194.4	89.0	1790	4	US-08-997-685A-11 Sequence 11, Appl
3	874.2	65.1	1512	4	US-09-086-436-32 Sequence 32, Appl
4	871	64.9	1584	4	US-08-997-685A-3 Sequence 3, Appl
5	751.8	56.0	2976	4	US-09-774-528-317 Sequence 317, Appl
6	735.2	54.8	2733	4	US-08-997-685A-1 Sequence 1, Appl
7	706	52.6	1518	4	US-09-086-436-34 Sequence 34, Appl
8	688.8	51.3	1507	4	US-08-997-685A-5 Sequence 5, Appl
9	680.2	50.7	2246	4	US-09-086-436-38 Sequence 38, Appl
10	680.2	50.7	2263	4	US-08-997-685A-9 Sequence 9, Appl
11	680.2	50.7	3224	4	US-09-774-528-238 Sequence 238, Appl
12	666.6	49.7	1307	3	US-09-172-422-3 Sequence 3, Appl
13	331.8	24.7	1083	4	US-09-270-767-1038 Sequence 1038, Appl
14	331.8	24.7	1083	4	US-09-270-767-1038 Sequence 1038, Appl
15	123.6	9.2	1040	4	US-09-086-436-36 Sequence 36, Appl
16	110	8.2	1060	4	US-08-997-685A-7 Sequence 7, Appl
17	102.6	7.6	3480	3	US-09-226-012-1 Sequence 1, Appl
18	102.6	7.6	3950	3	US-09-226-012-3 Sequence 3, Appl
19	86.6	6.5	3249	4	US-09-358-383C-3 Sequence 3, Appl
20	86.6	6.5	3355	4	US-09-358-383C-1 Sequence 1, Appl
21	85.4	6.4	3323	4	US-09-600-776-1 Sequence 1, Appl
22	83.8	6.2	3249	4	US-09-343-494-2 Sequence 2, Appl
23	83.8	6.2	3857	3	US-09-336-643A-19 Sequence 19, Appl
24	78.6	5.9	3041	4	US-09-694-777A-19 Sequence 19, Appl
25	70.8	5.3	2366	4	US-09-799-451-351 Sequence 351, Appl
26	63.8	4.8	2241	2	US-08-838-219B-20 Sequence 20, Appl
27	63.8	4.8	2241	3	US-09-233-336A-20 Sequence 20, Appl

28	63.8	4.8	2241	3	US-09-233-752A-20 Sequence 20, Appl
29	63.8	4.8	2241	4	US-09-402-036-20 Sequence 20, Appl
30	63.8	4.8	2241	4	US-09-904-226-20 Sequence 20, Appl
31	63.8	4.8	2370	2	US-08-838-219B-19 Sequence 19, Appl
32	63.8	4.8	2370	3	US-09-233-336A-19 Sequence 19, Appl
33	63.8	4.8	2370	3	US-09-233-752A-19 Sequence 19, Appl
34	63.8	4.8	2370	3	US-09-402-036-19 Sequence 19, Appl
35	63.8	4.8	2370	4	US-09-904-226-19 Sequence 19, Appl
36	63.8	4.8	2403	1	US-08-471-033-30 Sequence 30, Appl
37	63.8	4.8	2403	2	US-08-471-044-30 Sequence 30, Appl
38	63.8	4.8	2403	2	US-08-463-483A-30 Sequence 30, Appl
39	63.8	4.8	2403	2	US-08-471-046A-30 Sequence 30, Appl
40	63.8	4.8	2403	2	US-08-470-566B-30 Sequence 30, Appl
41	63.8	4.8	2403	2	US-08-838-219B-30 Sequence 30, Appl
42	63.8	4.8	2403	2	US-08-469-334-30 Sequence 30, Appl
43	63.8	4.8	2403	3	US-09-300-522-30 Sequence 30, Appl
44	63.8	4.8	2403	3	US-09-233-336A-7 Sequence 7, Appl
45	63.8	4.8	2403	3	US-09-233-752A-7 Sequence 7, Appl

## ALIGNMENTS

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RESULT 1
US-09-086-436-40
; Sequence 40, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandell, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbe, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; FILE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 1792
; TYPE: DNA
; ORGANISM: Human
US-09-086-436-40

Query Match      89.9%; Score 1207; DB 4; Length 1792;
Best Local Similarity 99.0%; Pred. No. 3.2e-238;
Matches 1235; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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541 TGGCTTACCAAGATCTCTGAGCTTCTGCGGCTGCTGCGCTTCTGACGCTGATCCGCT 600

64 ACATTCATAGAGGAGAGATCTTCCATACATGACCTGAGCGAGCGAGTATGA 123

601 ACATTCATAGAGGAGAGATCTTCCATACATGACCTGAGCGAGCGAGTATGA 660

124 GATCTGATCTCATCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183

661 GATCTGATCTCATCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

184 TCTGTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243

721 TCTGTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

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781 TGAACACCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840

304 TGGCTTACCAAGATCTCTGAGCTTCTGCGGCTGCTGCGCTTCTGACGCTGATCCGCT 363



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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:42:39 ; Search time 5779 Seconds  
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Title: US-09-640-582a-1  
Perfect score: 1342  
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Scoring table: IDENTITY NUC  
Gap 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: gb\_in:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARYS

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1	1335.6	99.5	1342	AX018991	AX018991 Sequence
2	1297	96.6	3372	AX211346	AX211346 Sequence
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4	1295.4	96.5	3459	AX348086	AX348086 Sequence
5	1295.4	96.5	3459	HS012582	HS012582 Homo sapi
6	1208	90.0	1792	AF064877	AF064877 Homo sapi
7	1207	89.9	1792	AR483555	AR483555 Sequence
8	1194.8	89.0	105108	AC139689	AC139689 Homo sapi
9	1194.8	89.0	133193	AC139548	AC139548 Homo sapi
10	1194.8	89.0	199198	AC021413	AC021413 Homo sapi
11	1194.4	89.0	1790	AR307665	AR307665 Sequence
12	1193.4	88.9	127422	BD139757	BD139757 Ion Chan
13	1193.2	88.9	163776	AC136294	AC136294 Homo sapi
14	1192.6	88.9	163776	AC135994	AC135994 Homo sapi
15	1191.6	88.8	2125	AX647819	AX647819 Sequence
16	1191.6	88.8	123089	AC135731	AC135731 Homo sapi
17	1191.6	88.8	123233	AC135625	AC135625 Homo sapi
18	1191.6	88.8	158033	AC135991	AC135991 Homo sapi
19	1191.6	88.8	164711	AC139564	AC139564 Homo sapi

C	20	1191.6	88.8	166484	2	AC026830	AC026830 Homo sapi
C	21	1191.6	88.8	184252	2	AC139565	AC139565 Homo sapi
C	22	1191.6	88.8	184448	2	AC139426	AC139426 Homo sapi
C	23	1101.2	82.1	1654	6	CO718501	CO718501 Sequence
C	24	1074.2	80.0	2633	10	AB164197	AB164197 Rattus no
C	25	1071	79.8	2511	10	AF247451	AF247451 Rattus no
C	26	1048.6	78.1	3102	6	AX211350	AX211350 Sequence
C	27	1048.6	78.1	3102	10	MM225122	MM225122 Mus muscu
C	28	1032.4	76.9	1820	6	AX018997	AX018997 Homo sapi
C	29	996	74.2	1031	9	AF064851	AF064851 Homo sapi
C	30	992.4	73.9	2866	6	AX019000	AX019000 Sequence
C	31	953.4	71.0	3737	4	AB022927	AB022927 Oryctolag
C	32	940.6	70.1	152040	2	AC139547	AC139547 Homo sapi
C	33	927.2	69.1	4751	6	AX019005	AX019005 Sequence
C	34	927.2	69.1	4751	6	AX348088	AX348088 Sequence
C	35	927.2	69.1	4751	6	HS013249	HS013249 Homo sapi
C	36	927.2	69.1	5065	9	HS013249	HS013249 Homo sapi
C	37	927.2	69.1	5065	9	HS013249	HS013249 Homo sapi
C	38	925.6	69.0	1933	6	CO715368	CO715368 Sequence
C	39	925.6	69.0	4333	6	CO729612	CO729612 Sequence
C	40	896.8	66.8	3993	10	AF247453	AF247453 Rattus no
C	41	874.2	65.1	1512	6	AR483551	AR483551 Sequence
C	42	874.2	65.1	1513	10	AF064873	AF064873 Mus muscu
C	43	871	64.9	1384	6	AR307661	AR307661 Sequence
C	44	871	64.9	1584	6	BD139756	BD139756 Ion Chan
C	45	763.8	56.9	3053	5	AF421883	AF421883 Oncorhynch

#### ALIGNMENTS

RESULT 1  
LOCUS AX018991 1342 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1 from Patent WO942574.  
ACCESSION AX018991  
VERSION AX018991.1 GI:10043084  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baumann, A., Gauss, R., Kaupp, B., Boenigk, W., Scholten, A. and Seifert, R.  
TITLE Sequences of an ionic channel and the use thereof  
JOURNAL Patient: WO 942574-A 1 26-AUG-1999.  
BAUMANN ARND (DE); GAUSS RENATE (DE); KAUPP BENJAMIN (DE); BOENIGK WOLFGANG (DE); KERNFORSCHUNGSANLAGE JUELICH (DE); SCHOLTEN ALEXANDER (DE); SEIFERT REINHARD (DE)

FEATURES  
source 1..1342  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

#### ORIGIN

Query Match 99.5%; Score 1335.6; DB 6; Length 1342;  
Best Local Similarity 100.0%; Pred. No. 1.4e-169;  
Matches 1342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGTTGGCTTACCAAGATCTCAGGCTCTGCGTGGCGCTTCAGCGCTGATCC	60
DB	1	CGTTGGCTTACCAAGATCTCAGGCTCTGCGTGGCGCTTCAGCGCTGATCC	60
QY	61	GCTACATCATGAGGAGAGATCTTCACATGACCTATGACCTGGCGAGGGGTGA	120
DB	61	GCTACATCATGAGGAGAGATCTTCACATGACCTATGACCTGGCGAGGGGTGA	120
QY	121	TGAGATCTGCATCTCATGAGATGCTGCTCTGCTGCACCTGGAGCGGCTGCTGC	180
DB	121	TGAGATCTGCATCTCATGAGATGCTGCTCTGCTGCACCTGGAGCGGCTGCTGC	180

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Run on: January 4, 2005, 13:44:53 ; Search time 705 Seconds  
(without alignments)  
9992.515 Million cell updates/sec

Title: US-09-640-582A-1

Perfect score: 1342

Sequence: 1 cgttcgctcaccacgaatc.....caccctgchcncctcaccc 1342

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 2: geneseqn190s:\*
- 3: geneseqn200s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335.6	99.5	1342	2	AAZ09482 Human Ih
2	1297	96.6	3372	2	AAH48729 Human HCN
3	1295.4	96.5	3459	2	AAZ09756 Human HCN
4	1194.4	89.0	1790	2	AAH84445 Human bra
5	1191.6	88.8	2125	10	ADC87558 Human GPC
6	1113.2	83.0	3431	4	AAH98302 Human EST
7	1048.6	78.1	3102	4	AAH48731 Human HC
8	1032.4	76.9	1820	2	AAZ09488 Bovine re
9	992.4	73.9	2886	2	AAZ09491 Human Ih
10	927.2	69.1	4751	2	AAZ09496 Human bra
11	927.2	69.1	4751	6	AAZ09757 Human HCN
12	927.2	69.1	5065	4	AAH48730 Human HCN
13	927.2	69.1	5065	4	AAH48730 Human HCN
14	871	64.9	1584	2	AAH84444 Mouse bra
15	753.4	56.1	3852	6	AAH44691 Human tra
16	753	56.1	2340	6	ABK6386 Human HCN
17	751.8	56.0	2317	8	ABX71090 Human HCN
18	751.8	56.0	2325	3	AAH6779 Human HCN
19	751.8	56.0	2325	3	ABZ75841 Human HCN
20	751.8	56.0	2325	8	ABZ58682 Human HCN
21	751.8	56.0	2325	8	ACA61916 CDNA enco

22	751.8	56.0	2325	10	ABX95515	ABX95515 CDNA enco
23	751.8	56.0	2346	6	AAZ29758	AAZ29758 Human HCN
24	751.4	56.0	2340	6	ABK6387	ABK6387 Human HCN
25	751.4	56.0	2340	6	ABK6385	ABK6385 Human HCN
26	735.2	54.8	2733	2	AAH84442	AAH84442 Mouse bra
27	720.8	53.7	3112	2	AAZ09483	AAZ09483 Rat olfac
28	688.8	51.3	1507	2	AAH84446	AAH84446 Mouse bra
29	681.8	50.8	2990	10	ADJ95123	ADJ95123 Novel NOV
30	680.2	50.7	1873	6	AAH18224	AAH18224 Human PCR
31	680.2	50.7	1873	6	AAH18223	AAH18223 Human PCR
32	680.2	50.7	2263	2	AAH84443	AAH84443 Human bra
33	680.2	50.7	2670	6	AAZ29755	AAZ29755 Human HCN
34	680.2	50.7	2673	8	ABZ75836	ABZ75836 Human HCN
35	680.2	50.7	2673	8	ABZ58677	ABZ58677 Human HCN
36	680.2	50.7	2673	8	ACA61911	ACA61911 CDNA enco
37	680.2	50.7	2673	10	ABX95510	ABX95510 CDNA enco
38	680.2	50.7	2748	6	ABT09623	ABT09623 Human HCN
39	680.2	50.7	2748	6	ABT09624	ABT09624 Human HCN
40	680.2	50.7	2748	6	ABT09630	ABT09630 Human HCN
41	680.2	50.7	2748	6	ABT09629	ABT09629 Human HCN
42	680.2	50.7	2748	6	ABT09631	ABT09631 Human HCN
43	680.2	50.7	2791	6	AAH18215	AAH18215 Human CDN
44	680.2	50.7	2791	6	AAH18213	AAH18213 Human CDN
45	680.2	50.7	2980	6	AAH18216	AAH18216 Human CDN

#### ALIGNMENTS

RESULT 1  
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ID AAZ09482 standard; DNA; 1342 BP.  
XX  
AC AAZ09482;  
XX  
DT 02-NOV-1999 (first entry)  
XX  
DE Human Ih ion channel DNA fragment.  
XX  
KW Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;  
KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;  
KW treatment; diagnosis; pacemaker; ion channel-related disease; cardiac disease;  
KW circulatory disorder; sinus ganglion regulation; sleep disorder;  
KW cortico-thalamic neuron; pain; detection; mutation; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO942574-A1.  
XX  
PD 26-AUG-1999.  
XX  
PF 12-FEB-1999; 99WO-EP000942.  
XX  
PR 17-FEB-1998; 98DE-01006581.  
XX  
PA (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.  
XX  
PI Baumann A, Boenigk W, Gauss R, Scholten A, Selfert R, Kaupp B,  
XX  
DR WPI, 1999-527472/44.  
XX  
PT New nucleic acid encoding an Ih ion channel, used to identify specific  
PT modulators, and for treatment, prevention and diagnosis of e.g. cardiac  
PT disease.  
XX  
PS Claim 3; Page 57; 82pp; German.  
XX  
CC This invention describes a novel Ih ion channel, isolated from human, sea  
CC urchin, bovine, rat, and fruitfly. The ion channels of the invention have  
CC analgesic and cardioactive activity. The Ih ion channel participates in  
CC the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid  
CC and its encoding protein is used to identify substances (A) that modulate  
CC activity of ion channels, to treat and/or diagnose ion channel-related

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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:46:04 ; Search time 4568 Seconds  
(without alignments)  
10705.368 Million cell updates/sec

Title: US-09-640-582a-1  
Perfect score: 1342  
Sequence: 1 cgttcgcttcaccacgaatc.....cacctgchgcncctcacc 1342

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1222.4	91.1	1794	3	BC039619 Homo sapi
2	736.8	54.9	913	6	CA488537 AGENCOURT
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4	719	53.6	3226	3	BC039156 Mus muscu
5	719	53.6	3265	3	AK032225 Mus muscu
6	719	53.6	4015	3	AK082719 Mus muscu
7	688.2	51.3	1620	9	AY399924 Homo sapi
8	687.4	51.2	815	2	BE546989 601071965
9	656.8	48.1	1638	9	AY399926 Mus muscu
10	646	48.1	786	4	BG974320 602844071
11	587	43.7	707	7	CK358214 AGENCOURT
12	585.2	43.6	691	2	AM073171 wY94102.x
13	541	40.3	564	6	CA842988
14	532.2	39.7	569	6	CB054837 NISC_gm06
15	532.2	39.7	569	6	CB054838 NISC_gm06
16	531.6	39.6	560	7	CK902966
17	527	39.3	595	2	BF593827 naC0502.
18	526.6	39.2	568	1	AI809833 wh7940.x
19	526	39.2	568	1	CK902965 1i27f10.x
20	523.6	39.0	659	6	CF253024 mdv004.b0
21	483	36.0	520	2	BF510959 UI-H-B14
22	473	35.2	957	6	BY714221 BY714221
23	471.4	35.1	1888	3	AK014722 Mus muscu
24	462.4	34.5	1120	5	BU956439 AGENCOURT

25	455.2	33.9	785	7	CN528592 UI-M-H00-
26	452.6	33.7	1620	9	AY399925 Pan trogl
27	451.8	33.7	780	2	BE260963 60151563
28	446.4	33.3	484	1	AI422949 tF23a05.x
29	443.6	33.1	453	6	CA842473 1i27f10.y
30	438.6	32.7	509	1	AA843373 aJ16b03.s
31	434.4	32.4	673	6	CB556893 AMGNNUC:N
32	433.8	32.3	954	6	CB8201579 AGENCOURT
33	429.8	32.0	702	7	CF531532 UI-M-FY0-
34	424.4	31.6	499	5	BK279829 BK279829
35	423.2	31.5	1087	2	BE798933 601583714
36	419.6	31.3	1263	9	AY401918 Mus muscu
37	416.8	31.1	858	4	BE793179 601581483
38	411.2	30.6	965	4	BI490063 603031668
39	411	30.6	785	5	BK872016 BK872016
40	403.4	30.1	974	5	BU914463 AGENCOURT
41	391.6	29.2	484	2	BE138253 UG50d03.Y
42	389.8	29.0	452	5	BK282916 BK282916
43	380.6	28.4	1266	9	AY401916 Homo sapi
44	379.2	28.3	1266	9	AY401917 Pan trogl
45	371.8	27.7	442	6	CB747868 AMGNNUC:N

## ALIGNMENTS

RESULT 1  
LOCUS BC039619  
DEFINITION Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 2, mRNA (CDNA clone IMAGE:5730201).  
ACCESSION BC039619  
VERSION 1  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
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